Seminar in Graduate Institute of Veterinary Microbiology, National Chung Hsing University

N-Linked Glycosylation Status of Classical Swine Fever Virus Strain Brescia E2 Glycoprotein Influences Virulence in Swine

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Classical swine fever is a highly contagious and fatal disease in pig. The causative agent is classical swine fever virus (CSFV) that is a member of the genus \textit{Pestivirus} of the family \textit{Flaviviridae}. The CSFV genome contains a single open reading frame encoding a 3,898 amino-acid polyprotein which through cellular and viral protease process into a mature protein.(1)

The surface structure of CSFV is composed of three glycoproteins, E\textsuperscript{ms}, E1 and E2. E2 is the most immunogenic glycoprotein and it has been implicated along with E\textsuperscript{ms} and E1, in viral adsorption to host cell. Now it has been known E2 of the CSFV strain Brescia has five putative N-linked sites and one putative O-linked glycosylation site. Predicted E2 glycosylation sites are highly conserved among CSFV strains. Glycosylation of E\textsuperscript{ms}, E1 or E2 may play an important role for receptor binding, membrane fusion, penetration and replication cycle. However, the function of added oligosaccharides is unknown. (2)(3)

In this study, the author used oligonucleotide site-directed mutagenesis of the highly virulent CSFV strain Brescia E2 gene to construct a panel of glycosylation mutants and these mutants were used to study the glycosylation sites on E2 glycoprotein to see whether they affect viral infectivity and virulence in swine. The authors found that the rescure of viable virus was completely impaired by removal of all putative glycosylation sites in E2 but when residue N185 was reverted, it's viral viability was not affected. Aside from the single mutation in E2, the N116A will turn to attenuated virus (N1v) that could decrease virus replication and shedding in infected swine.

Reference: